



1

GEN-T112XC1

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Chumakov, Ilya

<120> Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)

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<222> 67820..67848

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<222> 67941..67969

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<222> 67940..67969

<223> 5-169-331_T_S

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<222> 67709..67738

<223> 5-169-97_C_AS complement

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<222> 67707..67737

<223> 5-169-97_C_S

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<222> 67709..67738

<223> 5-169-97_G_AS complement

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<222> 67707..67737

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<222> 68199..68228

<223> 5-170-238_A_AS complement

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<222> 68198..68227

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<222> 68199..68228

<223> 5-170-238_G_AS complement

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<222> 68198..68227

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<223> 99-1572-578_C_AS complement

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<222> 67215..67247

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tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg att atg      521
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Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile
      125      130      135
tat ggc aaa gtg aat att cac tca att ggt ttt agc ttc agc tcg gac      665
Tyr Gly Lys Val Asn Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp
      140      145      150      155
tta caa agt acc caa gca tct agt ctg gaa ctg aca gag ata agt aga      713
Leu Gln Ser Thr Gln Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg
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Asp Ser Thr Val Asn His Thr Leu Thr Cys Thr Lys Ile Pro Pro Met
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Lys His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile Asn
      335      340      345
gga gac atc cac tta ctg gaa gta agg agc tgg tag cctacctaca      1287
Gly Asp Ile His Leu Leu Glu Val Arg Ser Trp *
      350      355
cagctgctac aaaaaccaa atacagaatg gcttctgtga tactggcctt gctgaaacgc      1347
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gggggcagca acatttatag ccagttaaag ccactctgcc ctctctccta ctttggtgta      1527
ctcttcaaga atgccattca acaagtatgt atggagtacc tactataata cagtagctaa      1587
catgtattga gcacagatgt tttttggtaa aactgtgagg agctaggata tatacttggt      1647
gaaacaaacc agtatgttcc ctgttctctt gagcttcgac tcttctgtgc tctattgctg      1707

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cgcactgctt	tttctacagg	cattacatca	actcctaagg	ggtcctctgg	gattagttaa	1767
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ctcaaataat	caggaggtgg	tcacttcgca	acttgcctcc	tcacccaac	tcaaaacagg	4947
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taagaaagga atggattctg gtagcaagac aatataattc tcctttagtt tttcagccag 5187
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tgttttccaa actgtgtccc aggactgcaa atctttaatg tgaaatgtct ttttataatc 5487
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<221> polyA_signal
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<223> 5-2-162 : polymorphic base A or T

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<221> allele
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<223> 5-3-84 : polymorphic base A or G

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<223> 5-10-39 : polymorphic base C or T

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taacctttaa atgaaacttg cctaaaatct taggtcatat acagaagaga ctccaatcga      180
caagaagctg gaaaagaatg atg ttg tcc tta aac aac cta cag aat atc atc      233
                Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile
                1                5                10
tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag ctg gat      281
Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp
                15                20                25
cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac gca gac      329
Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp Ala Asp
                30                35                40
aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct cga gcc      377
Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala
                45                50                55
gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc tgc att      425
Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile
        60                65                70                75
gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag atc acc      473
Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr
                80                85                90
tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg att atg      521
Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met
                95                100                105
gtg cta aag gac aaa ttc cag gtg gct gta aat gga aaa cat act ctg      569
Val Leu Lys Asp Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu
                110                115                120
ctc tat ggc cac agg atc ggc cca gag aaa ata gac act ctg ggc att      617
Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile
                125                130                135
tat ggc aaa gtg aat att cac tca att ggt ttt agc ttc agc tcg gac      665
Tyr Gly Lys Val Asn Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp
        140                145                150                155
tta caa agt acc caa gca tct agt ctg gaa ctg aca gag ata agt aga      713
Leu Gln Ser Thr Gln Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg
                160                165                170
gaa aat gtt cca aag tct ggc acg ccc cag ctt agc ctg cca ttc gct      761
Glu Asn Val Pro Lys Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala
                175                180                185
gca agg ttg aac acc ccc atg ggc cct gga cga act gtc gtc gtt aaa      809
Ala Arg Leu Asn Thr Pro Met Gly Pro Gly Arg Thr Val Val Val Lys
                190                195                200
gga gaa gtg aat gca aat gcc aaa agc ttt aat gtt gac cta cta gca      857
Gly Glu Val Asn Ala Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala
                205                210                215
gga aaa tca aag gat att gct cta cac ttg aac cca cgc ctg aat att      905
Gly Lys Ser Lys Asp Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile
        220                225                230                235
aaa gca ttt gta aga aat tct ttt ctt cag gag tcc tgg gga gaa gaa      953
Lys Ala Phe Val Arg Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu
                240                245                250
gag aga aat att acc tct ttc cca ttt agt cct ggg atg tac ttt gag      1001
Glu Arg Asn Ile Thr Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu
                255                260                265
atg ata att tac tgt gat gtt aga gaa ttc aag gtt gca gta aat ggc      1049

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Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly
    270          275          280
gta cac agc ctg gag tac aaa cac aga ttt aaa gag ctc agc agt att    1097
Val His Ser Leu Glu Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile
    285          290          295
gac acg ctg gaa att aat gga gac atc cac tta ctg gaa caa tca ttc    1145
Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu Leu Glu Gln Ser Phe
    300          305          310          315
aat caa aag agt gaa atg aag cac att aac aaa gca gga ggc gcc acg    1193
Asn Gln Lys Ser Glu Met Lys His Ile Asn Lys Ala Gly Gly Ala Thr
    320          325          330
gac cgc ctc cct cca cac cgc tcc ttc cgc ctt cat tcc ttg ccc aca    1241
Asp Arg Leu Pro Pro His Arg Ser Phe Arg Leu His Ser Leu Pro Thr
    335          340          345
ggc ttg cac tgg aag ctg aat aag aat ccc caa aac tca aac ttc cta    1289
Gly Leu His Trp Lys Leu Asn Lys Asn Pro Gln Asn Ser Asn Phe Leu
    350          355          360
ggg atg cca ccc ctt tag tagctcacac ctccccctc caagagctaa    1337
Gly Met Pro Pro Leu *
    365
gaaacaaagg agaatgtact tttgtagctt agataagcaa tgaatcagta aaggactgat    1397
ctacttgctc caccacccct cccttaataa taacatttac tggtatttcc tgggcctaag    1457
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<211> 316

<212> PRT

<213> Homo sapiens

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<221> VARIANT

<222> 18

<223> 5-2-162 : polymorphic amino acid Tyr or Phe

<221> VARIANT

<222> 35

<223> 5-2-213 : polymorphic amino acid Cys or Arg

<221> VARIANT

<222> 55

<223> 5-3-84 : polymorphic amino acid Val or Met

<221> VARIANT

<222> 183

<223> 5-7-195 : polymorphic amino acid Ser or Arg

<400> 5

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          20          25          30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
          35          40          45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
          50          55          60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65          70          75          80
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
          85          90          95
Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
          100         105         110
Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
          115         120         125
Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
          130         135         140
Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
145         150         155         160
Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
          165         170         175
Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr
          180         185         190
Pro Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val Asn Ala
          195         200         205
Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser Lys Asp
          210         215         220
Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe Val Arg
225         230         235         240
Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu Arg Asn Ile Thr
          245         250         255
Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys
          260         265         270
Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu
          275         280         285
Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile
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Asn Gly Asp Ile His Leu Leu Glu Val Arg Ser Trp
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<210> 6

<211> 358

<212> PRT

<213> Homo sapiens

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 <221> VARIANT
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 <223> 5-2-213 : polymorphic amino acid Cys or Arg

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 <223> 5-3-84 : polymorphic amino acid Val or Met

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 <223> 5-202-95 : polymorphic amino acid Asp or Tyr

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 <222> 211
 <223> 5-202-117 : polymorphic amino acid Leu or Stop

 <221> VARIANT
 <222> 225
 <223> 5-7-195 : polymorphic amino acid Ser or Arg

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 Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
 35 40 45
 Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
 50 55 60
 Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
 65 70 75 80
 Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
 85 90 95
 Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
 100 105 110
 Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
 115 120 125
 Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
 130 135 140
 Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
 145 150 155 160
 Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
 165 170 175
 Ser Gly Thr Pro Gln Leu Pro Ser Asn Arg Gly Gly Asp Ile Ser Lys
 180 185 190
 Ile Ala Pro Arg Thr Val Tyr Thr Lys Ser Lys Asp Ser Thr Val Asn
 195 200 205
 His Thr Leu Thr Cys Thr Lys Ile Pro Pro Met Asn Tyr Val Ser Lys
 210 215 220


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Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr Pro Met Gly Pro Gly Arg
225                230                235                240
Thr Val Val Val Lys Gly Glu Val Asn Ala Asn Ala Lys Ser Phe Asn
                245                250                255
Val Asp Leu Leu Ala Gly Lys Ser Lys Asp Ile Ala Leu His Leu Asn
                260                265                270
Pro Arg Leu Asn Ile Lys Ala Phe Val Arg Asn Ser Phe Leu Gln Glu
                275                280                285
Ser Trp Gly Glu Glu Glu Arg Asn Ile Thr Ser Phe Pro Phe Ser Pro
                290                295                300
Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys
305                310                315                320
Val Ala Val Asn Gly Val His Ser Leu Glu Tyr Lys His Arg Phe Lys
                325                330                335
Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu
                340                345                350
Leu Glu Val Arg Ser Trp
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<210> 7

<211> 368

<212> PRT

<213> Homo sapiens

<220>

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<223> 5-2-162 : polymorphic amino acid Tyr or Phe

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<222> 35

<223> 5-2-213 : polymorphic amino acid Cys or Arg

<221> VARIANT

<222> 55

<223> 5-3-84 : polymorphic amino acid Val or Met

<221> VARIANT

<222> 183

<223> 5-7-195 : polymorphic amino acid Ser or Arg

<400> 7

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Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile
1                5                10                15
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                20                25                30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
                35                40                45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
                50                55                60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65                70                75                80
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
                85                90                95

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Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
 100 105 110
 Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
 115 120 125
 Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
 130 135 140
 Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
 145 150 155 160
 Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
 165 170 175
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<222> (8187)..(34266)

<223> n=a, g, c or t

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<223> polymorphic base; y=C or T

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1          5          10          15
Thr Leu Lys Ile Thr Gly Ser Ile Ala Asp Gly Thr Asp Gly Phe Val
          20          25          30
Ile Asn Leu Gly Gln Gly Thr Asp Lys Leu Asn Leu His Phe Asn Pro
          35          40          45
Arg Phe Ser Glu Ser Thr Ile Val Cys Asn Ser Leu Asp Gly Ser Asn
          50          55          60
Trp Gly Gln Glu Gln Arg Glu Asp His Leu Cys Phe Ser Pro Gly Ser
65          70          75          80
Glu Val Lys Phe Thr Val Thr Phe Glu Ser Asp Lys Phe Lys Val Lys
          85          90          95
Leu Pro Asp Gly His Glu Leu Thr Phe Pro Asn Arg Leu Gly His Ser
          100         105         110
His Leu Ser Tyr Leu Ser Val Arg Gly Gly Phe Asn Met Ser Ser Phe
          115         120         125
Lys Leu Lys Glu
          130

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<210> 14

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(134)

<223> amino acid sequence of leg1

<400> 14

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Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys
1          5          10          15
Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu
          20          25          30
Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg
          35          40          45
Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp
          50          55          60
Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln
65          70          75          80
Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu
          85          90          95
Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu
          100         105         110
Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile
          115         120         125
Lys Cys Val Ala Phe Asp
          130

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<210> 15
 <211> 316
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(316)
 <223> amino acid sequence of PCTA

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 1 5 10 15
 Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
 20 25 30
 Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
 35 40 45
 Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
 50 55 60
 Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
 65 70 75 80
 Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
 85 90 95
 Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
 100 105 110
 Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
 115 120 125
 Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
 130 135 140
 Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
 145 150 155 160
 Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
 165 170 175
 Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr
 180 185 190
 Pro Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val Asn Ala
 195 200 205
 Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser Lys Asp
 210 215 220
 Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe Val Arg
 225 230 235 240
 Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu Glu Arg Asn Ile Thr
 245 250 255
 Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys
 260 265 270
 Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu
 275 280 285
 Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile
 290 295 300
 Asn Gly Asp Ile His Leu Leu Glu Val Arg Ser Trp
 305 310 315

<210> 16
 <211> 358

<212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(358)

<223> amino acid sequence of PCTA.var

<400> 16

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Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
           20          25          30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
           35          40          45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
           50          55          60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65          70          75          80
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
           85          90          95
Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
           100         105         110
Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
           115         120         125
Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
           130         135         140
Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
145         150         155         160
Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
           165         170         175
Ser Gly Thr Pro Gln Leu Pro Ser Asn Arg Gly Gly Asp Ile Ser Lys
           180         185         190
Ile Ala Pro Arg Thr Val Tyr Thr Lys Ser Lys Asp Ser Thr Val Asn
           195         200         205
His Thr Leu Thr Cys Thr Lys Ile Pro Pro Met Asn Tyr Val Ser Lys
           210         215         220
Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr Pro Met Gly Pro Gly Arg
225         230         235         240
Thr Val Val Val Lys Gly Glu Val Asn Ala Asn Ala Lys Ser Phe Asn
           245         250         255
Val Asp Leu Leu Ala Gly Lys Ser Lys Asp Ile Ala Leu His Leu Asn
           260         265         270
Pro Arg Leu Asn Ile Lys Ala Phe Val Arg Asn Ser Phe Leu Gln Glu
           275         280         285
Ser Trp Gly Glu Glu Glu Arg Asn Ile Thr Ser Phe Pro Phe Ser Pro
           290         295         300
Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys
305         310         315         320
Val Ala Val Asn Gly Val His Ser Leu Glu Tyr Lys His Arg Phe Lys
           325         330         335
Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu
           340         345         350
Leu Glu Val Arg Ser Trp
           355

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<210> 17
 <211> 315
 <212> PRT
 <213> Mus musculus

<220>
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 <222> (1)..(315)
 <223> amino acid sequence of PCTA.mus

<400> 17
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 1 5 10 15
 Pro Tyr Val Gly Thr Ile Thr Glu Gln Leu Lys Pro Gly Ser Leu Ile
 20 25 30
 Val Ile Arg Gly His Val Pro Lys Asp Ser Glu Arg Phe Gln Val Asp
 35 40 45
 Phe Gln Leu Gly Asn Ser Leu Lys Pro Arg Ala Asp Val Ala Phe His
 50 55 60
 Phe Asn Pro Arg Phe Lys Arg Ser Ser Cys Ile Val Cys Asn Thr Leu
 65 70 75 80
 Thr Gln Glu Lys Trp Gly Trp Glu Glu Ile Thr Tyr Asp Met Pro Phe
 85 90 95
 Arg Lys Glu Lys Ser Phe Glu Ile Val Phe Met Val Leu Lys Asn Lys
 100 105 110
 Phe Gln Val Ala Val Asn Gly Arg His Val Leu Leu Tyr Ala His Arg
 115 120 125
 Ile Ser Pro Glu Gln Ile Asp Thr Val Gly Ile Tyr Gly Lys Val Asn
 130 135 140
 Ile His Ser Ile Gly Phe Arg Phe Ser Ser Asp Leu Gln Ser Met Glu
 145 150 155 160
 Thr Ser Ala Leu Gly Leu Thr Gln Ile Asn Arg Glu Asn Ile Gln Lys
 165 170 175
 Pro Gly Lys Leu Gln Leu Ser Leu Pro Phe Glu Ala Arg Leu Asn Ala
 180 185 190
 Ser Met Gly Pro Gly Arg Thr Val Val Ile Lys Gly Glu Val Asn Thr
 195 200 205
 Asn Ala Arg Ser Phe Asn Val Asp Leu Val Ala Gly Lys Thr Arg Asp
 210 215 220
 Ile Ala Leu His Leu Asn Pro Arg Leu Asn Lys Ala Phe Val Arg Asn
 225 230 235 240
 Ser Phe Leu Gln Asp Ala Trp Gly Glu Glu Glu Arg Asn Ile Thr Cys
 245 250 255
 Phe Pro Phe Ser Ser Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys Asp
 260 265 270
 Val Arg Glu Phe Lys Val Ala Ile Asn Gly Val His Ser Leu Glu Tyr
 275 280 285
 Lys His Arg Phe Lys Asp Leu Ser Ser Ile Asp Thr Leu Ser Val Asp
 290 295 300
 Gly Asp Ile Arg Leu Leu Asp Val Arg Ser Trp
 305 310 315

<210> 18
 <211> 355
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(355)
 <223> amino acid sequence of gal9-1

<400> 18
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 20 25 30
 Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
 35 40 45
 Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
 50 55 60
 Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
 65 70 75 80
 Ser Trp Gly Pro Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
 85 90 95
 Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
 100 105 110
 Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
 115 120 125
 His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
 130 135 140
 Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser
 145 150 155 160
 Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly
 165 170 175
 Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
 180 185 190
 Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
 195 200 205
 Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
 210 215 220
 Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
 225 230 235 240
 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
 245 250 255
 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
 260 265 270
 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
 275 280 285
 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
 290 295 300
 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
 305 310 315 320
 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
 325 330 335
 Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
 340 345 350

Val Gln Thr
355

<210> 19
<211> 323
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(323)
<223> amino acid sequence of gal

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20 25 30
Val Asn Gly Thr Val Leu Ser Ser Gly Thr Arg Phe Ala Val Asn
35 40 45
Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
50 55 60
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65 70 75 80
Ser Trp Gly Pro Glu Glu Arg Arg Thr His Met Pro Phe Gln Lys Gly
85 90 95
Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100 105 110
Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125
His Arg Val Asp Thr Ile Phe Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140
Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145 150 155 160
Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
165 170 175
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
180 185 190
Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
195 200 205
Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
210 215 220
Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Leu Arg Phe
225 230 235 240
Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
245 250 255
Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
260 265 270
Ser Phe Ser Val Trp Ile Leu Cys Gly Ala His Cys Leu Lys Val Ala
275 280 285
Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
290 295 300
Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
305 310 315 320

Val Gln Thr

<210> 20
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(135)
 <223> amino acid sequence of leg7

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 Ser Asn Val Pro His Lys Ser Ser Leu Pro Glu Gly Ile Arg Pro Gly
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 Thr Val Leu Arg Ile Arg Gly Leu Val Pro Pro Asn Ala Ser Arg Phe
 20 25 30
 His Val Asn Leu Leu Cys Gly Glu Gln Gly Ser Asp Ala Ala Leu
 35 40 45
 His Phe Asn Pro Arg Leu Asp Thr Ser Glu Val Val Phe Asn Ser Lys
 50 55 60
 Glu Gln Gly Ser Trp Gly Arg Glu Glu Arg Gly Pro Gly Val Pro Phe
 65 70 75 80
 Gln Arg Gly Gln Pro Phe Glu Val Leu Ile Ile Ala Ser Asp Asp Gly
 85 90 95
 Phe Lys Ala Val Val Gly Asp Ala Gln Tyr His His Phe Arg His Arg
 100 105 110
 Leu Pro Leu Ala Arg Val Arg Leu Val Glu Val Gly Gly Asp Val Gln
 115 120 125
 Leu Asp Ser Val Arg Ile Phe
 130 135

<210> 21
 <211> 323
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(323)
 <223> amino acid sequence of gal4

<400> 21
 Met Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr
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 Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser
 20 25 30
 Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val
 35 40 45
 Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe
 50 55 60
 Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln
 65 70 75 80


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Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys
      85                      90                      95
Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr
      100                      105                      110
Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu
      115                      120                      125
Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
      130                      135                      140
Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
      145                      150                      155                      160
Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
      165                      170                      175
Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
      180                      185                      190
Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
      195                      200                      205
Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
      210                      215                      220
Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
      225                      230                      235                      240
Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
      245                      250                      255
Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
      260                      265                      270
Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
      275                      280                      285
Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
      290                      295                      300
Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
      305                      310                      315                      320
Val Gln Ile

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<210> 22
<211> 466
<212> PRT
<213> Artificial Sequence

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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110
 Xaa Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Ile Pro Xaa Gly Leu Xaa Pro
 115 120 125
 Gly Xaa Xaa Xaa Xaa Ile Xaa Gly Xaa Val Xaa Pro Xaa Xaa Ala Xaa
 130 135 140
 Arg Phe Xaa Val Asn Leu Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa
 145 150 155 160
 Asp Xaa Ala Phe His Phe Asn Pro Arg Phe Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175
 Xaa Xaa Val Val Cys Asn Thr Xaa Xaa Xaa Gly Xaa Trp Gly Xaa Glu
 180 185 190
 Glu Arg Xaa Xaa Xaa Pro Phe Xaa Xaa Gly Xaa Xaa Phe Glu Xaa
 195 200 205
 Xaa Xaa Xaa Val Xaa Xaa Asp Xaa Phe Lys Val Xaa Val Asn Gly Xaa
 210 215 220
 Xaa Xaa Xaa Xaa Tyr Xaa His Arg Leu Xaa Pro Leu Xaa Xaa Val Xaa
 225 230 235 240
 Xaa Xaa Xaa Val Xaa Gly Asp Val Gln Leu Xaa Ser Ile Xaa Phe Xaa
 245 250 255
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 275 280 285
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 290 295 300
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 305 310 315 320
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa
 325 330 335
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

			340					345				350			
Gly	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		355					360				365				
Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Ala	Xaa	His	Xaa	Asn	Xaa	Arg	Xaa	Xaa	Xaa
		370				375					380				
Xaa	Xaa	Xaa	Val	Arg	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Gly	Xaa	Glu
385					390					395					400
Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Phe	Xaa	Xaa	Gly	Xaa	Xaa	Phe
				405					410					415	
Xaa	Xaa	Xaa	Ile	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Val	Xaa	Xaa	Xaa
			420					425					430		
Gly	Xaa	His	Xaa	Xaa	Xaa	Xaa	Xaa	His	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		435					440					445			
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Gly	Asp	Xaa	Xaa	Leu	Xaa	Xaa	Val	Xaa
		450				455					460				
Xaa	Xaa														
465															